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SEQUENCE LISTING

<110> Furuichi, Yasuhiro
 Hoshino, Tatsuo
 Kimura, Hitoshi
 Kiyasu, Tatsuya
 Nagahashi, Yoshie

<120> BIOTIN BIOSYNTHETIC GENES

<130> Biotin Genes

<140> 08/935,263

<141> 1997-09-22

<150> EP 96115540.5

<151> 1996-09-27

<160> 23

<170> PatentIn Ver. 2.1

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<213> Kurthia sp.

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 Thr Val Ala Thr Ser Leu Leu Tyr Met Ser Leu Gln Thr Met Gly Lys

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agc gtc aca ata ttt aag ccg ttt caa aca gga ttg att cac gaa acg 144
 Ser Val Thr Ile Phe Lys Pro Phe Gln Thr Gly Leu Ile His Glu Thr

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aat aca tac cct gac atc tct tgg ttt gag cag gaa ctt ggt gta aag 192
 Asn Thr Tyr Pro Asp Ile Ser Trp Phe Glu Gln Glu Leu Gly Val Lys

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gca cct ggg ttt tac atg ctt gaa ccc gaa aca tct cca cac tta gct	240
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65 70 75 80	
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Ile Lys Leu Thr Gly Gln Gln Ile Asp Glu Gln Lys Val Val Glu Arg	
85 90 95	
gtt cac gaa ctc gaa caa atg tat gac atc gtg tta gtc gag ggc gct	336
Val His Glu Leu Glu Gln Met Tyr Asp Ile Val Leu Val Glu Gly Ala	
100 105 110	
ggg gga ttg gcc gta cca ctc att gaa cga gcg aac agt ttc tat atg	384
Gly Gly Leu Ala Val Pro Leu Ile Glu Arg Ala Asn Ser Phe Tyr Met	
115 120 125	
aca acc gat tta att aga gat tgc aac atg cca gtc att ttc gtt tct	432
Thr Thr Asp Leu Ile Arg Asp Cys Asn Met Pro Val Ile Phe Val Ser	
130 135 140	
aca agc ggt tta gga tcg att cat aat gtc ata act acg cat tcg tat	480
Thr Ser Gly Leu Gly Ser Ile His Asn Val Ile Thr Thr His Ser Tyr	
145 150 155 160	
gcc aaa ttg cat gat att agc gtt aaa act att tta tat aac cat tat	528
Ala Lys Leu His Asp Ile Ser Val Lys Thr Ile Leu Tyr Asn His Tyr	
165 170 175	
cgg ccc gac gat gaa att cat cgt gac aat atc cta acc gtt gaa aag	576
Arg Pro Asp Asp Glu Ile His Arg Asp Asn Ile Leu Thr Val Glu Lys	
180 185 190	
ctc aca gga ctc gct gac ctc gcc tgc ata cca aca ttt gtc gac gta	624
Leu Thr Gly Leu Ala Asp Leu Ala Cys Ile Pro Thr Phe Val Asp Val	
195 200 205	
aga aaa gat ctg aga gtc tac ata ctt gat tta ctt agt aat cat gaa	672
Arg Lys Asp Leu Arg Val Tyr Ile Leu Asp Leu Leu Ser Asn His Glu	
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<213> Kurthia sp.

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Ser Val Thr Ile Phe Lys Pro Phe Gln Thr Gly Leu Ile His Glu Thr
35 40 45

Asn Thr Tyr Pro Asp Ile Ser Trp Phe Glu Gln Glu Leu Gly Val Lys
50 55 60

Ala Pro Gly Phe Tyr Met Leu Glu Pro Glu Thr Ser Pro His Leu Ala
65 70 75 80

Ile Lys Leu Thr Gly Gln Gln Ile Asp Glu Gln Lys Val Val Glu Arg
85 90 95

Val His Glu Leu Glu Gln Met Tyr Asp Ile Val Leu Val Glu Gly Ala
100 105 110

Gly Gly Leu Ala Val Pro Leu Ile Glu Arg Ala Asn Ser Phe Tyr Met
115 120 125

Thr Thr Asp Leu Ile Arg Asp Cys Asn Met Pro Val Ile Phe Val Ser
130 135 140

Thr Ser Gly Leu Gly Ser Ile His Asn Val Ile Thr Thr His Ser Tyr
145 150 155 160

Ala Lys Leu His Asp Ile Ser Val Lys Thr Ile Leu Tyr Asn His Tyr
165 170 175

Arg Pro Asp Asp Glu Ile His Arg Asp Asn Ile Leu Thr Val Glu Lys
180 185 190

Leu Thr Gly Leu Ala Asp Leu Ala Cys Ile Pro Thr Phe Val Asp Val
195 200 205

Arg Lys Asp Leu Arg Val Tyr Ile Leu Asp Leu Leu Ser Asn His Glu
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Phe Thr Gln Gln Leu Lys Glu Val Phe Lys Asn Glu
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gaa cgc ggg gaa ggg agc tac ctt ttt gac ata gaa ggc aat cgg tac 144
Glu Arg Gly Glu Gly Ser Tyr Leu Phe Asp Ile Glu Gly Asn Arg Tyr
35 40 45

ttg gac ggt tat gct tca tta tgg gtc aac gta cat ggc cat aat gaa 192
Leu Asp Gly Tyr Ala Ser Leu Trp Val Asn Val His Gly His Asn Glu
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cca gag cta aac aac gct ctc att gaa caa gtt gaa aaa gtc gca cac 240
Pro Glu Leu Asn Asn Ala Leu Ile Glu Gln Val Glu Lys Val Ala His
65 70 75 80

tca aca cta cta gga tct gca aat gta cca tcc ata tta ctg gct aag 288
Ser Thr Leu Leu Gly Ser Ala Asn Val Pro Ser Ile Leu Leu Ala Lys
85 90 95

aaa tta gca gag att act cct ggt cat tta tcg aaa gtc ttt tac tcg 336
Lys Leu Ala Glu Ile Thr Pro Gly His Leu Ser Lys Val Phe Tyr Ser
100 105 110

gac act gga tca gct gct gta gaa atc tcc ctt aaa gtc gct tat caa 384
Asp Thr Gly Ser Ala Ala Val Glu Ile Ser Leu Lys Val Ala Tyr Gln
115 120 125

tat tgg aaa aat atc gat cct gta aag tat caa cat aaa aat aaa ttt 432
Tyr Trp Lys Asn Ile Asp Pro Val Lys Tyr Gln His Lys Asn Lys Phe
130 135 140

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Val	Gly	Gly	Met	Asp	Leu	Phe	His	Arg	Ile	Phe	Lys	Pro	Leu	Leu	Phe	
				165					170						175	
gaa	cgg	att	cca	act	cct	tct	cct	tat	aca	tat	cgc	atg	gct	aaa	cac	576
Glu	Arg	Ile	Pro	Thr	Pro	Ser	Pro	Tyr	Thr	Tyr	Arg	Met	Ala	Lys	His	
			180						185					190		
ggg	gat	caa	gaa	gca	gtg	aaa	aac	tat	tgt	att	gat	gag	ctg	gaa	aag	624
Gly	Asp	Gln	Glu	Ala	Val	Lys	Asn	Tyr	Cys	Ile	Asp	Glu	Leu	Glu	Lys	
		195					200					205				
ttg	ctt	caa	gac	caa	gca	gag	gaa	att	gca	gga	ttg	att	atc	gaa	ccg	672
Leu	Leu	Gln	Asp	Gln	Ala	Glu	Glu	Ile	Ala	Gly	Leu	Ile	Ile	Glu	Pro	
	210					215					220					
ctt	gtt	caa	gga	gca	gca	ggc	atc	att	acc	cac	cct	cct	ggc	ttt	tta	720
Leu	Val	Gln	Gly	Ala	Ala	Gly	Ile	Ile	Thr	His	Pro	Pro	Gly	Phe	Leu	
225					230					235					240	
aaa	gcg	gtc	gaa	caa	ttg	tgc	aag	aag	tac	aat	ata	tta	ttg	att	tgt	768
Lys	Ala	Val	Glu	Gln	Leu	Cys	Lys	Lys	Tyr	Asn	Ile	Leu	Leu	Ile	Cys	
				245					250						255	
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Asp	Glu	Val	Ala	Val	Gly	Phe	Gly	Arg	Thr	Gly	Thr	Leu	Phe	Ala	Cys	
			260					265					270			
gaa	caa	gaa	gat	gtc	gtc	cct	gat	att	atg	tgt	atc	ggt	aaa	gga	att	864
Glu	Gln	Glu	Asp	Val	Val	Pro	Asp	Ile	Met	Cys	Ile	Gly	Lys	Gly	Ile	
		275					280					285				
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Thr	Gly	Gly	Tyr	Met	Pro	Leu	Ala	Ala	Thr	Ile	Met	Asn	Glu	Gln	Ile	
	290					295					300					
ttt	aat	tct	ttt	tta	gga	gag	ccc	gat	gaa	cat	aaa	acc	ttc	tat	cac	960
Phe	Asn	Ser	Phe	Leu	Gly	Glu	Pro	Asp	Glu	His	Lys	Thr	Phe	Tyr	His	
305					310					315					320	
ggc	cac	acc	tac	aca	ggg	aat	caa	cta	gcc	tgt	gcc	ctg	gcg	ctg	aag	1008
Gly	His	Thr	Tyr	Thr	Gly	Asn	Gln	Leu	Ala	Cys	Ala	Leu	Ala	Leu	Lys	
				325					330					335		

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 340 345 350

aaa tcc aag cag cta tct gaa aaa ctg caa tcg cta tat gaa ctc ccg 1104
 Lys Ser Lys Gln Leu Ser Glu Lys Leu Gln Ser Leu Tyr Glu Leu Pro
 355 360 365

att gtc ggt gat atc cgc cag cgc ggc ctc atg att gga ata gaa atc 1152
 Ile Val Gly Asp Ile Arg Gln Arg Gly Leu Met Ile Gly Ile Glu Ile
 370 375 380

gtt aaa gat cgc caa aca aaa gaa ccg ttc aca atc caa gaa aat atc 1200
 Val Lys Asp Arg Gln Thr Lys Glu Pro Phe Thr Ile Gln Glu Asn Ile
 385 390 395 400

gtt tca agc atc atc caa aac gct cgg gaa aat ggc ctg atc att cgg 1248
 Val Ser Ser Ile Ile Gln Asn Ala Arg Glu Asn Gly Leu Ile Ile Arg
 405 410 415

gaa ctt ggc cct gtc atc aca atg atg ccc att ctt tcc atg tca gaa 1296
 Glu Leu Gly Pro Val Ile Thr Met Met Pro Ile Leu Ser Met Ser Glu
 420 425 430

aag gaa ctg aat act atg gtc gaa act gtc tac cgt tcg ata cag gac 1344
 Lys Glu Leu Asn Thr Met Val Glu Thr Val Tyr Arg Ser Ile Gln Asp
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<213> Kurthia sp.

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 35 40 45

Leu Asp Gly Tyr Ala Ser Leu Trp Val Asn Val His Gly His Asn Glu
50 55 60

Pro Glu Leu Asn Asn Ala Leu Ile Glu Gln Val Glu Lys Val Ala His
65 70 75 80

Ser Thr Leu Leu Gly Ser Ala Asn Val Pro Ser Ile Leu Leu Ala Lys
85 90 95

Lys Leu Ala Glu Ile Thr Pro Gly His Leu Ser Lys Val Phe Tyr Ser
100 105 110

Asp Thr Gly Ser Ala Ala Val Glu Ile Ser Leu Lys Val Ala Tyr Gln
115 120 125

Tyr Trp Lys Asn Ile Asp Pro Val Lys Tyr Gln His Lys Asn Lys Phe
130 135 140

Val Ser Leu Asn Glu Ala Tyr His Gly Asp Thr Val Gly Ala Val Ser
145 150 155 160

Val Gly Gly Met Asp Leu Phe His Arg Ile Phe Lys Pro Leu Leu Phe
165 170 175

Glu Arg Ile Pro Thr Pro Ser Pro Tyr Thr Tyr Arg Met Ala Lys His
180 185 190

Gly Asp Gln Glu Ala Val Lys Asn Tyr Cys Ile Asp Glu Leu Glu Lys
195 200 205

Leu Leu Gln Asp Gln Ala Glu Glu Ile Ala Gly Leu Ile Ile Glu Pro
210 215 220

Leu Val Gln Gly Ala Ala Gly Ile Ile Thr His Pro Pro Gly Phe Leu
225 230 235 240

Lys Ala Val Glu Gln Leu Cys Lys Lys Tyr Asn Ile Leu Leu Ile Cys
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Asp Glu Val Ala Val Gly Phe Gly Arg Thr Gly Thr Leu Phe Ala Cys
260 265 270

Glu Gln Glu Asp Val Val Pro Asp Ile Met Cys Ile Gly Lys Gly Ile
275 280 285

Thr Gly Gly Tyr Met Pro Leu Ala Ala Thr Ile Met Asn Glu Gln Ile
290 295 300

Phe Asn Ser Phe Leu Gly Glu Pro Asp Glu His Lys Thr Phe Tyr His
 305 310 315 320

Gly His Thr Tyr Thr Gly Asn Gln Leu Ala Cys Ala Leu Ala Leu Lys
 325 330 335

Asn Ile Glu Leu Ile Glu Arg Arg Asp Leu Val Lys Asp Ile Gln Lys
 340 345 350

Lys Ser Lys Gln Leu Ser Glu Lys Leu Gln Ser Leu Tyr Glu Leu Pro
 355 360 365

Ile Val Gly Asp Ile Arg Gln Arg Gly Leu Met Ile Gly Ile Glu Ile
 370 375 380

Val Lys Asp Arg Gln Thr Lys Glu Pro Phe Thr Ile Gln Glu Asn Ile
 385 390 395 400

Val Ser Ser Ile Ile Gln Asn Ala Arg Glu Asn Gly Leu Ile Ile Arg
 405 410 415

Glu Leu Gly Pro Val Ile Thr Met Met Pro Ile Leu Ser Met Ser Glu
 420 425 430

Lys Glu Leu Asn Thr Met Val Glu Thr Val Tyr Arg Ser Ile Gln Asp
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50	55	60	
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Arg Phe Gly Thr Gly Ser Thr Gly Ser Arg Leu Thr Thr Gly Asn Thr			
65	70	75	80
att gtc cat gaa aaa cta gag aaa aga ctt gca gag ttt aag caa acg			288
Ile Val His Glu Lys Leu Glu Lys Arg Leu Ala Glu Phe Lys Gln Thr			
85	90	95	
gat gca gcg ata gta tta aac aca ggg tat atg gct aac ata gca gcg			336
Asp Ala Ala Ile Val Leu Asn Thr Gly Tyr Met Ala Asn Ile Ala Ala			
100	105	110	
tta acg acc ctt gtt ggt agt gac gat ctc att tta tcc gat gag atg			384
Leu Thr Thr Leu Val Gly Ser Asp Asp Leu Ile Leu Ser Asp Glu Met			
115	120	125	
aat cat gcc agt att att gat ggc tgc cgt tta tca cgt gcg gaa act			432
Asn His Ala Ser Ile Ile Asp Gly Cys Arg Leu Ser Arg Ala Glu Thr			
130	135	140	
atc att tat cgt cat gct gat tta ctt gac ttg gaa atg aaa ctc cag			480
Ile Ile Tyr Arg His Ala Asp Leu Leu Asp Leu Glu Met Lys Leu Gln			
145	150	155	160
att aat acc cgc tac agg aaa aga ata att gta acg gat ggc gtc ttt			528
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165	170	175	
tcg atg gat ggt gat att gcg cca ttg cca ggt att gtc gaa ctt gcc			576
Ser Met Asp Gly Asp Ile Ala Pro Leu Pro Gly Ile Val Glu Leu Ala			
180	185	190	
aag cgt tat gat gca ctt gtt atg gtg gat gac gca cat gcg acg ggt			624
Lys Arg Tyr Asp Ala Leu Val Met Val Asp Asp Ala His Ala Thr Gly			
195	200	205	
gtt tta ggt aaa gac gga agg gga act tct gaa cat ttt gga ctg aag			672
Val Leu Gly Lys Asp Gly Arg Gly Thr Ser Glu His Phe Gly Leu Lys			

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Glu Gly Gly Tyr Ile Ala Gly Ser Arg Ser Leu Val Asp Tyr Val Leu			
	245	250	255
aat cga gcc aga ccg ttt gtc ttc tct acc gcc tta tca gca gga gta			816
Asn Arg Ala Arg Pro Phe Val Phe Ser Thr Ala Leu Ser Ala Gly Val			
	260	265	270
gta gca agt gca ctt aca gca gtc gat atc att caa tca gaa cct gaa			864
Val Ala Ser Ala Leu Thr Ala Val Asp Ile Ile Gln Ser Glu Pro Glu			
	275	280	285
cgc aga gta cgc att cga gcc atg agc cag cgt ctt tat aat gaa tta			912
Arg Arg Val Arg Ile Arg Ala Met Ser Gln Arg Leu Tyr Asn Glu Leu			
	290	295	300
acc tcc ctt ggc tac aca gtt tcg ggg gga gaa act ccg att ctt gcc			960
Thr Ser Leu Gly Tyr Thr Val Ser Gly Gly Glu Thr Pro Ile Leu Ala			
	305	310	315
att att tgc gga gaa ccg gaa cag gcc atg ttc ctt tcg aaa gaa tta			1008
Ile Ile Cys Gly Glu Pro Glu Gln Ala Met Phe Leu Ser Lys Glu Leu			
	325	330	335
cat aag cac gga att tat gca cca gct atc cgt tcg cca acg gta cct			1056
His Lys His Gly Ile Tyr Ala Pro Ala Ile Arg Ser Pro Thr Val Pro			
	340	345	350
ctt gga act tcg cgc att cga ctt acg tta atg gcg aca cat caa gaa			1104
Leu Gly Thr Ser Arg Ile Arg Leu Thr Leu Met Ala Thr His Gln Glu			
	355	360	365
gaa caa atg aat cat gtt atc gac gtg ttc aga aca atc ctt acc aat			1152
Glu Gln Met Asn His Val Ile Asp Val Phe Arg Thr Ile Leu Thr Asn			
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aga tac aaa tag			1164
Arg Tyr Lys			
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<213> Kurthia sp.

<400> 6

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35 40 45

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50 55 60

Arg Phe Gly Thr Gly Ser Thr Gly Ser Arg Leu Thr Thr Gly Asn Thr
65 70 75 80

Ile Val His Glu Lys Leu Glu Lys Arg Leu Ala Glu Phe Lys Gln Thr
85 90 95

Asp Ala Ala Ile Val Leu Asn Thr Gly Tyr Met Ala Asn Ile Ala Ala
100 105 110

Leu Thr Thr Leu Val Gly Ser Asp Asp Leu Ile Leu Ser Asp Glu Met
115 120 125

Asn His Ala Ser Ile Ile Asp Gly Cys Arg Leu Ser Arg Ala Glu Thr
130 135 140

Ile Ile Tyr Arg His Ala Asp Leu Leu Asp Leu Glu Met Lys Leu Gln
145 150 155 160

Ile Asn Thr Arg Tyr Arg Lys Arg Ile Ile Val Thr Asp Gly Val Phe
165 170 175

Ser Met Asp Gly Asp Ile Ala Pro Leu Pro Gly Ile Val Glu Leu Ala
180 185 190

Lys Arg Tyr Asp Ala Leu Val Met Val Asp Asp Ala His Ala Thr Gly
195 200 205

Val Leu Gly Lys Asp Gly Arg Gly Thr Ser Glu His Phe Gly Leu Lys
210 215 220

Gly Lys Ile Asp Ile Glu Met Gly Thr Leu Ser Lys Ala Val Gly Ala

225 230 235 240
 Glu Gly Gly Tyr Ile Ala Gly Ser Arg Ser Leu Val Asp Tyr Val Leu
 245 250 255
 Asn Arg Ala Arg Pro Phe Val Phe Ser Thr Ala Leu Ser Ala Gly Val
 260 265 270
 Val Ala Ser Ala Leu Thr Ala Val Asp Ile Ile Gln Ser Glu Pro Glu
 275 280 285
 Arg Arg Val Arg Ile Arg Ala Met Ser Gln Arg Leu Tyr Asn Glu Leu
 290 295 300
 Thr Ser Leu Gly Tyr Thr Val Ser Gly Gly Glu Thr Pro Ile Leu Ala
 305 310 315 320
 Ile Ile Cys Gly Glu Pro Glu Gln Ala Met Phe Leu Ser Lys Glu Leu
 325 330 335
 His Lys His Gly Ile Tyr Ala Pro Ala Ile Arg Ser Pro Thr Val Pro
 340 345 350
 Leu Gly Thr Ser Arg Ile Arg Leu Thr Leu Met Ala Thr His Gln Glu
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 Arg Tyr Lys
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 <213> Kurthia sp.

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Lys Met Leu Ala Glu Asn Val Ile Lys Gly Tyr Lys Val Thr Ala Glu	
20 25 30	
gaa gca ctt gct att gta caa gca cct gac aac gag gtt tta gag att	144
Glu Ala Leu Ala Ile Val Gln Ala Pro Asp Asn Glu Val Leu Glu Ile	
35 40 45	
ttg aat gca gct ttc ctt att cgt cag cac tat tat gga aaa aag gtt	192
Leu Asn Ala Ala Phe Leu Ile Arg Gln His Tyr Tyr Gly Lys Lys Val	
50 55 60	
aaa ttg aat atg atc att aat acg aag tca ggt cta tgt cct gaa gat	240
Lys Leu Asn Met Ile Ile Asn Thr Lys Ser Gly Leu Cys Pro Glu Asp	
65 70 75 80	
tgt ggc tat tgt tcg cag tca atc gtg tcg gaa gct cct atc gat aaa	288
Cys Gly Tyr Cys Ser Gln Ser Ile Val Ser Glu Ala Pro Ile Asp Lys	
85 90 95	
tat gct tgg ctg acc aaa gag aag att gtt gaa ggt gct caa gaa tca	336
Tyr Ala Trp Leu Thr Lys Glu Lys Ile Val Glu Gly Ala Gln Glu Ser	
100 105 110	
att cgt cgc aaa gct ggc acg tat tgt atc gtt gct tct ggc cgt cgt	384
Ile Arg Arg Lys Ala Gly Thr Tyr Cys Ile Val Ala Ser Gly Arg Arg	
115 120 125	
ccg acc aat agg gaa att gat cat gtc att gaa gct gtg aaa gaa att	432
Pro Thr Asn Arg Glu Ile Asp His Val Ile Glu Ala Val Lys Glu Ile	
130 135 140	
cgc gag aca acg gat ctt aaa ata tgc tgc tgt cta ggt ttc tta aat	480
Arg Glu Thr Thr Asp Leu Lys Ile Cys Cys Cys Leu Gly Phe Leu Asn	
145 150 155 160	
gaa acg cat gcc agt aag cta gct gaa gct ggg gtt cat cgc tac aag	528
Glu Thr His Ala Ser Lys Leu Ala Glu Ala Gly Val His Arg Tyr Lys	
165 170 175	
cac aac tta aat aca tct caa gat aat tat aag aat att aca tcc aca	576
His Asn Leu Asn Thr Ser Gln Asp Asn Tyr Lys Asn Ile Thr Ser Thr	
180 185 190	
cat act tat gag gac cgt gta gat aca gtc gaa gct gta aaa gag gcc	624
His Thr Tyr Glu Asp Arg Val Asp Thr Val Glu Ala Val Lys Glu Ala	
195 200 205	

gga atg tct cca tgc tgc ggt gcc att ttt ggt atg aat gag tct aat 672
 Gly Met Ser Pro Cys Ser Gly Ala Ile Phe Gly Met Asn Glu Ser Asn
 210 215 220

gaa gaa gca gta gag att gcc cta tcc cta cgc agt ctt gac gcg gat 720
 Glu Glu Ala Val Glu Ile Ala Leu Ser Leu Arg Ser Leu Asp Ala Asp
 225 230 235 240

tct att cct tgt aat ttc ctc aat gcg att gac ggt aca cca ctt gag 768
 Ser Ile Pro Cys Asn Phe Leu Asn Ala Ile Asp Gly Thr Pro Leu Glu
 245 250 255

gga act tcc gag ttg act cca act aaa tgt ttg aaa tta att tgc atg 816
 Gly Thr Ser Glu Leu Thr Pro Thr Lys Cys Leu Lys Leu Ile Ser Met
 260 265 270

atg aga ttt gtt aat cca agt aag gaa atc cgt ctt gct gga ggt cgc 864
 Met Arg Phe Val Asn Pro Ser Lys Glu Ile Arg Leu Ala Gly Gly Arg
 275 280 285

gag gtg aac ctc cgt tcc atg caa ccc atg gca ctt tat gca gcc aat 912
 Glu Val Asn Leu Arg Ser Met Gln Pro Met Ala Leu Tyr Ala Ala Asn
 290 295 300

tct atc ttc gtc ggc gat tat cta aca aca gct gga caa gaa cct acg 960
 Ser Ile Phe Val Gly Asp Tyr Leu Thr Thr Ala Gly Gln Glu Pro Thr
 305 310 315 320

gcg gat tgg ggc att atc gaa gac ctt ggt ttt gaa att gaa gaa tgc 1008
 Ala Asp Trp Gly Ile Ile Glu Asp Leu Gly Phe Glu Ile Glu Glu Cys
 325 330 335

gct ctt taa 1017
 Ala Leu

<210> 8

<211> 338

<212> PRT

<213> Kurthia sp.

<400> 8

Met Arg Lys Glu Gly Leu Gly Leu Glu Thr Leu Val Lys Lys Asp Trp
 1 5 10 15

Lys Met Leu Ala Glu Asn Val Ile Lys Gly Tyr Lys Val Thr Ala Glu
 20 25 30

Glu	Ala	Leu	Ala	Ile	Val	Gln	Ala	Pro	Asp	Asn	Glu	Val	Leu	Glu	Ile	35	40	45
Leu	Asn	Ala	Ala	Phe	Leu	Ile	Arg	Gln	His	Tyr	Tyr	Gly	Lys	Lys	Val	50	55	60
Lys	Leu	Asn	Met	Ile	Ile	Asn	Thr	Lys	Ser	Gly	Leu	Cys	Pro	Glu	Asp	65	70	75 80
Cys	Gly	Tyr	Cys	Ser	Gln	Ser	Ile	Val	Ser	Glu	Ala	Pro	Ile	Asp	Lys	85	90	95
Tyr	Ala	Trp	Leu	Thr	Lys	Glu	Lys	Ile	Val	Glu	Gly	Ala	Gln	Glu	Ser	100	105	110
Ile	Arg	Arg	Lys	Ala	Gly	Thr	Tyr	Cys	Ile	Val	Ala	Ser	Gly	Arg	Arg	115	120	125
Pro	Thr	Asn	Arg	Glu	Ile	Asp	His	Val	Ile	Glu	Ala	Val	Lys	Glu	Ile	130	135	140
Arg	Glu	Thr	Thr	Asp	Leu	Lys	Ile	Cys	Cys	Cys	Leu	Gly	Phe	Leu	Asn	145	150	155 160
Glu	Thr	His	Ala	Ser	Lys	Leu	Ala	Glu	Ala	Gly	Val	His	Arg	Tyr	Lys	165	170	175
His	Asn	Leu	Asn	Thr	Ser	Gln	Asp	Asn	Tyr	Lys	Asn	Ile	Thr	Ser	Thr	180	185	190
His	Thr	Tyr	Glu	Asp	Arg	Val	Asp	Thr	Val	Glu	Ala	Val	Lys	Glu	Ala	195	200	205
Gly	Met	Ser	Pro	Cys	Ser	Gly	Ala	Ile	Phe	Gly	Met	Asn	Glu	Ser	Asn	210	215	220
Glu	Glu	Ala	Val	Glu	Ile	Ala	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Ala	Asp	225	230	235 240
Ser	Ile	Pro	Cys	Asn	Phe	Leu	Asn	Ala	Ile	Asp	Gly	Thr	Pro	Leu	Glu	245	250	255
Gly	Thr	Ser	Glu	Leu	Thr	Pro	Thr	Lys	Cys	Leu	Lys	Leu	Ile	Ser	Met	260	265	270
Met	Arg	Phe	Val	Asn	Pro	Ser	Lys	Glu	Ile	Arg	Leu	Ala	Gly	Gly	Arg	275	280	285

Glu Val Asn Leu Arg Ser Met Gln Pro Met Ala Leu Tyr Ala Ala Asn
 290 295 300

Ser Ile Phe Val Gly Asp Tyr Leu Thr Thr Ala Gly Gln Glu Pro Thr
 305 310 315 320

Ala Asp Trp Gly Ile Ile Glu Asp Leu Gly Phe Glu Ile Glu Glu Cys
 325 330 335

Ala Leu

<210> 9

<211> 804

<212> DNA

<213> Kurthia sp.

<220>

<221> CDS

<222> (1)..(801)

<400> 9

atg cca ttc gta aat cat gac aat gaa agc ctt tac tat gag gtt cac 48
 Met Pro Phe Val Asn His Asp Asn Glu Ser Leu Tyr Tyr Glu Val His
 1 5 10 15

gga caa ggt gat cct tta ttg ttg att atg ggg ctc ggc tat aac tct 96
 Gly Gln Gly Asp Pro Leu Leu Leu Ile Met Gly Leu Gly Tyr Asn Ser
 20 25 30

tta tcc tgg cat aga acg gtg ccc act tta gct aag cgc ttt aaa gta 144
 Leu Ser Trp His Arg Thr Val Pro Thr Leu Ala Lys Arg Phe Lys Val
 35 40 45

atc gtt ttt gat aat cgt ggt gtt ggt aag agc agt aag cct gaa cag 192
 Ile Val Phe Asp Asn Arg Gly Val Gly Lys Ser Ser Lys Pro Glu Gln
 50 55 60

cca tat tct att gaa atg atg gct gag gat gca aga gcg gtc ctt gat 240
 Pro Tyr Ser Ile Glu Met Met Ala Glu Asp Ala Arg Ala Val Leu Asp
 65 70 75 80

gct gtt tcg gtt gac tca gca cat gta tat ggg att tca atg ggt gga 288
 Ala Val Ser Val Asp Ser Ala His Val Tyr Gly Ile Ser Met Gly Gly
 85 90 95

atg att gcc caa agg ctg gca atc aca tat cca gaa cgt gtt cgt tct	336
Met Ile Ala Gln Arg Leu Ala Ile Thr Tyr Pro Glu Arg Val Arg Ser	
100 105 110	

ctt gtt cta ggt tgt acc act gcg ggt ggt act act cat att caa cct	384
Leu Val Leu Gly Cys Thr Thr Ala Gly Gly Thr Thr His Ile Gln Pro	
115 120 125	

tct cca gaa ata tct act tta atg gta tct cga gcc tcc ctt aca ggt	432
Ser Pro Glu Ile Ser Thr Leu Met Val Ser Arg Ala Ser Leu Thr Gly	
130 135 140	

tct cca agg gat aat gcc tgg tta gcg gca cca ata gtt tat agt caa	480
Ser Pro Arg Asp Asn Ala Trp Leu Ala Ala Pro Ile Val Tyr Ser Gln	
145 150 155 160	

gct ttt att gag aag cac cct gaa tta att cag gaa gat atc caa aag	528
Ala Phe Ile Glu Lys His Pro Glu Leu Ile Gln Glu Asp Ile Gln Lys	
165 170 175	

cga ata gaa atc att act ccg cca agc gcc tat ctg tct caa cta caa	576
Arg Ile Glu Ile Ile Thr Pro Pro Ser Ala Tyr Leu Ser Gln Leu Gln	
180 185 190	

gct tgt cta act cat gat aca tcc aat gaa ctt gat aaa ata aac ata	624
Ala Cys Leu Thr His Asp Thr Ser Asn Glu Leu Asp Lys Ile Asn Ile	
195 200 205	

cca aca ttg att ata cac ggt gat gca gat aat ttg gtt cca tat gaa	672
Pro Thr Leu Ile Ile His Gly Asp Ala Asp Asn Leu Val Pro Tyr Glu	
210 215 220	

aac ggt aaa atg tta gct gaa cgt att cag ggt tct cag ttt cac acc	720
Asn Gly Lys Met Leu Ala Glu Arg Ile Gln Gly Ser Gln Phe His Thr	
225 230 235 240	

gta tcc tgt gct ggc cac att tat tta aca gaa gca gct aag gaa gca	768
Val Ser Cys Ala Gly His Ile Tyr Leu Thr Glu Ala Ala Lys Glu Ala	
245 250 255	

aat gac aaa gtt ata cag ttt cta gct cat cta taa	804
Asn Asp Lys Val Ile Gln Phe Leu Ala His Leu	
260 265	

<210> 10

<211> 267

<212> PRT

<213> Kurthia sp.

<400> 10

Met Pro Phe Val Asn His Asp Asn Glu Ser Leu Tyr Tyr Glu Val His
1 5 10 15

Gly Gln Gly Asp Pro Leu Leu Leu Ile Met Gly Leu Gly Tyr Asn Ser
20 25 30

Leu Ser Trp His Arg Thr Val Pro Thr Leu Ala Lys Arg Phe Lys Val
35 40 45

Ile Val Phe Asp Asn Arg Gly Val Gly Lys Ser Ser Lys Pro Glu Gln
50 55 60

Pro Tyr Ser Ile Glu Met Met Ala Glu Asp Ala Arg Ala Val Leu Asp
65 70 75 80

Ala Val Ser Val Asp Ser Ala His Val Tyr Gly Ile Ser Met Gly Gly
85 90 95

Met Ile Ala Gln Arg Leu Ala Ile Thr Tyr Pro Glu Arg Val Arg Ser
100 105 110

Leu Val Leu Gly Cys Thr Thr Ala Gly Gly Thr Thr His Ile Gln Pro
115 120 125

Ser Pro Glu Ile Ser Thr Leu Met Val Ser Arg Ala Ser Leu Thr Gly
130 135 140

Ser Pro Arg Asp Asn Ala Trp Leu Ala Ala Pro Ile Val Tyr Ser Gln
145 150 155 160

Ala Phe Ile Glu Lys His Pro Glu Leu Ile Gln Glu Asp Ile Gln Lys
165 170 175

Arg Ile Glu Ile Ile Thr Pro Pro Ser Ala Tyr Leu Ser Gln Leu Gln
180 185 190

Ala Cys Leu Thr His Asp Thr Ser Asn Glu Leu Asp Lys Ile Asn Ile
195 200 205

Pro Thr Leu Ile Ile His Gly Asp Ala Asp Asn Leu Val Pro Tyr Glu
210 215 220

Asn Gly Lys Met Leu Ala Glu Arg Ile Gln Gly Ser Gln Phe His Thr
225 230 235 240

Val Ser Cys Ala Gly His Ile Tyr Leu Thr Glu Ala Ala Lys Glu Ala
245 250 255

Asn Asp Lys Val Ile Gln Phe Leu Ala His Leu
260 265

<210> 11

<211> 1197

<212> DNA

<213> Kurthia sp.

<220>

<221> CDS

<222> (1)..(1194)

<400> 11

atg cac agt gaa aaa caa tta cct tgt tgg gaa gaa aaa att aag aaa 48
Met His Ser Glu Lys Gln Leu Pro Cys Trp Glu Glu Lys Ile Lys Lys
1 5 10 15

gaa ctg gct tat tta gaa gag ata tcg caa aaa cgt gaa ctc gtt tca 96
Glu Leu Ala Tyr Leu Glu Glu Ile Ser Gln Lys Arg Glu Leu Val Ser
20 25 30

acg gaa ttc gcc gag cag cca tgg ctt atg atc aac ggg tgc aag atg 144
Thr Glu Phe Ala Glu Gln Pro Trp Leu Met Ile Asn Gly Cys Lys Met
35 40 45

cta aat cta gct tct aat aac tat tta gga tat gca ggg gat gag cgg 192
Leu Asn Leu Ala Ser Asn Asn Tyr Leu Gly Tyr Ala Gly Asp Glu Arg
50 55 60

ctg aaa aag gct atg gta gat gca gta cat aca tat ggt gca gga gcg 240
Leu Lys Lys Ala Met Val Asp Ala Val His Thr Tyr Gly Ala Gly Ala
65 70 75 80

acg gct tca cgt tta att att ggc aat cac cct ctt tac gag caa gca 288
Thr Ala Ser Arg Leu Ile Ile Gly Asn His Pro Leu Tyr Glu Gln Ala
85 90 95

gaa caa gct ctt gtc aat tgg aag aaa gcc gaa gca gga ctc att att 336
Glu Gln Ala Leu Val Asn Trp Lys Lys Ala Glu Ala Gly Leu Ile Ile
100 105 110

aac agt gga tat aac gcg aac ctt gga att atc tcc acc ttg ctg tcc 384
Asn Ser Gly Tyr Asn Ala Asn Leu Gly Ile Ile Ser Thr Leu Leu Ser

115	120	125	
cgt aac gat att att tat agc gat aaa ttg aat cat gca agc att gtc			432
Arg Asn Asp Ile Ile Tyr Ser Asp Lys Leu Asn His Ala Ser Ile Val			
130	135	140	
gat gga gct ctc tta agc cgt gca aag cat cta cgc tat cgt cat aat			480
Asp Gly Ala Leu Leu Ser Arg Ala Lys His Leu Arg Tyr Arg His Asn			
145	150	155	160
gat tta gat cat tta gaa gca tta ttg aaa aaa tca tcg atg gaa gca			528
Asp Leu Asp His Leu Glu Ala Leu Leu Lys Lys Ser Ser Met Glu Ala			
165	170	175	
cgt aaa tta att gtg acg gat acg gtc ttc agc atg gac ggt gac ttt			576
Arg Lys Leu Ile Val Thr Asp Thr Val Phe Ser Met Asp Gly Asp Phe			
180	185	190	
gct tat ctt gaa gac ctt gtt cgg tta aaa gaa cgt tat aac gct atg			624
Ala Tyr Leu Glu Asp Leu Val Arg Leu Lys Glu Arg Tyr Asn Ala Met			
195	200	205	
tta atg aca gat gaa gca cac gga agc ggc atc tac ggt aaa aac ggt			672
Leu Met Thr Asp Glu Ala His Gly Ser Gly Ile Tyr Gly Lys Asn Gly			
210	215	220	
gaa ggt tat gcc ggt cat ctc cat ctt caa aat aaa ata gat atc caa			720
Glu Gly Tyr Ala Gly His Leu His Leu Gln Asn Lys Ile Asp Ile Gln			
225	230	235	240
atg gga aca ttc agt aaa gcg ctc ggt tca ttc ggg gcc tat gtc gtc			768
Met Gly Thr Phe Ser Lys Ala Leu Gly Ser Phe Gly Ala Tyr Val Val			
245	250	255	
ggg aaa aaa tgg ctc atc gac tat tta aaa aat cgc atg cgc gga ttc			816
Gly Lys Lys Trp Leu Ile Asp Tyr Leu Lys Asn Arg Met Arg Gly Phe			
260	265	270	
ata tat tca act gca ctc ccc ccg gcc ata ctc ggt gct atg aaa aca			864
Ile Tyr Ser Thr Ala Leu Pro Pro Ala Ile Leu Gly Ala Met Lys Thr			
275	280	285	
gcg ata gaa ctt gta cag caa gaa cca gaa cgc cgc tca ctg ctc caa			912
Ala Ile Glu Leu Val Gln Gln Glu Pro Glu Arg Arg Ser Leu Leu Gln			
290	295	300	
aca cat tca gaa cac ttt aga gaa gaa ctc aca tat tac ggg ttt aat			960
Thr His Ser Glu His Phe Arg Glu Glu Leu Thr Tyr Tyr Gly Phe Asn			

305	310	315	320	
att tgt gga agt cga tca caa att gtt cct atc gtc atc ggg gaa aac				1008
Ile Cys Gly Ser Arg Ser Gln Ile Val Pro Ile Val Ile Gly Glu Asn				
	325	330	335	
gaa aaa gcg atg gaa ttt gcc aca cgt ttg cag aaa gaa gga att gca				1056
Glu Lys Ala Met Glu Phe Ala Thr Arg Leu Gln Lys Glu Gly Ile Ala				
	340	345	350	
gct att gct gtc agg ccg ccg acc gtt cct gaa aat gag gcg aga atc				1104
Ala Ile Ala Val Arg Pro Pro Thr Val Pro Glu Asn Glu Ala Arg Ile				
	355	360	365	
cgt ttt act gta aca gct ctc cac gat aaa aaa gat ctt gat tgg gca				1152
Arg Phe Thr Val Thr Ala Leu His Asp Lys Lys Asp Leu Asp Trp Ala				
	370	375	380	
gtt gaa aaa gtt tcg atc att gga aaa gaa atg ggt gtt att taa				1197
Val Glu Lys Val Ser Ile Ile Gly Lys Glu Met Gly Val Ile				
385	390	395		
 <210> 12				
<211> 398				
<212> PRT				
<213> Kurthia sp.				
 <400> 12				
Met His Ser Glu Lys Gln Leu Pro Cys Trp Glu Glu Lys Ile Lys Lys				
1	5	10	15	
Glu Leu Ala Tyr Leu Glu Glu Ile Ser Gln Lys Arg Glu Leu Val Ser				
20	25	30		
Thr Glu Phe Ala Glu Gln Pro Trp Leu Met Ile Asn Gly Cys Lys Met				
35	40	45		
Leu Asn Leu Ala Ser Asn Asn Tyr Leu Gly Tyr Ala Gly Asp Glu Arg				
50	55	60		
Leu Lys Lys Ala Met Val Asp Ala Val His Thr Tyr Gly Ala Gly Ala				
65	70	75	80	
Thr Ala Ser Arg Leu Ile Ile Gly Asn His Pro Leu Tyr Glu Gln Ala				
85	90	95		
Glu Gln Ala Leu Val Asn Trp Lys Lys Ala Glu Ala Gly Leu Ile Ile				

100	105	110
Asn Ser Gly Tyr Asn Ala Asn Leu Gly Ile Ile Ser Thr Leu Leu Ser		
115	120	125
Arg Asn Asp Ile Ile Tyr Ser Asp Lys Leu Asn His Ala Ser Ile Val		
130	135	140
Asp Gly Ala Leu Leu Ser Arg Ala Lys His Leu Arg Tyr Arg His Asn		
145	150	155 160
Asp Leu Asp His Leu Glu Ala Leu Leu Lys Lys Ser Ser Met Glu Ala		
165	170	175
Arg Lys Leu Ile Val Thr Asp Thr Val Phe Ser Met Asp Gly Asp Phe		
180	185	190
Ala Tyr Leu Glu Asp Leu Val Arg Leu Lys Glu Arg Tyr Asn Ala Met		
195	200	205
Leu Met Thr Asp Glu Ala His Gly Ser Gly Ile Tyr Gly Lys Asn Gly		
210	215	220
Glu Gly Tyr Ala Gly His Leu His Leu Gln Asn Lys Ile Asp Ile Gln		
225	230	235 240
Met Gly Thr Phe Ser Lys Ala Leu Gly Ser Phe Gly Ala Tyr Val Val		
245	250	255
Gly Lys Lys Trp Leu Ile Asp Tyr Leu Lys Asn Arg Met Arg Gly Phe		
260	265	270
Ile Tyr Ser Thr Ala Leu Pro Pro Ala Ile Leu Gly Ala Met Lys Thr		
275	280	285
Ala Ile Glu Leu Val Gln Gln Glu Pro Glu Arg Arg Ser Leu Leu Gln		
290	295	300
Thr His Ser Glu His Phe Arg Glu Glu Leu Thr Tyr Tyr Gly Phe Asn		
305	310	315 320
Ile Cys Gly Ser Arg Ser Gln Ile Val Pro Ile Val Ile Gly Glu Asn		
325	330	335
Glu Lys Ala Met Glu Phe Ala Thr Arg Leu Gln Lys Glu Gly Ile Ala		
340	345	350
Ala Ile Ala Val Arg Pro Pro Thr Val Pro Glu Asn Glu Ala Arg Ile		

355

360

365

Arg Phe Thr Val Thr Ala Leu His Asp Lys Lys Asp Leu Asp Trp Ala
 370 375 380

Val Glu Lys Val Ser Ile Ile Gly Lys Glu Met Gly Val Ile
 385 390 395

<210> 13

<211> 747

<212> DNA

<213> Kurthia sp.

<220>

<221> CDS

<222> (1) .. (744)

<400> 13

atg aaa cag ccg aat tta gtc atg ctt cct ggc tgg gga atg gaa aaa 48
 Met Lys Gln Pro Asn Leu Val Met Leu Pro Gly Trp Gly Met Glu Lys
 1 5 10 15

gat gcg ttt caa ccg tta atc aaa ccg ctg tca gaa gta ttt cac ctc 96
 Asp Ala Phe Gln Pro Leu Ile Lys Pro Leu Ser Glu Val Phe His Leu
 20 25 30

tca ttc ata gaa tgg aga gat atg aaa aca cta aat gac ttt gaa gaa 144
 Ser Phe Ile Glu Trp Arg Asp Met Lys Thr Leu Asn Asp Phe Glu Glu
 35 40 45

cga gtc ata gac aca atc gct tct att gat ggt cct gtt ttt tta ctt 192
 Arg Val Ile Asp Thr Ile Ala Ser Ile Asp Gly Pro Val Phe Leu Leu
 50 55 60

ggc tgg tca tta gga tct cta tta tca ctt gaa ctt gta agt tcg tat 240
 Gly Trp Ser Leu Gly Ser Leu Leu Ser Leu Glu Leu Val Ser Ser Tyr
 65 70 75 80

cga gaa aaa ata aaa ggt ttt ata cta att ggc gca aca agt cgt ttt 288
 Arg Glu Lys Ile Lys Gly Phe Ile Leu Ile Gly Ala Thr Ser Arg Phe
 85 90 95

acc aca gga gat aat tat tca ttt ggc tgg gat cca cga atg gtc gag 336
 Thr Thr Gly Asp Asn Tyr Ser Phe Gly Trp Asp Pro Arg Met Val Glu
 100 105 110

cgc atg aag aaa caa ctg cag cgc aat aaa gag aag act ttg act tct 384
 Arg Met Lys Lys Gln Leu Gln Arg Asn Lys Glu Lys Thr Leu Thr Ser
 115 120 125

ttc tat gaa gca atg ttt tcc gaa gct gaa aaa gaa gaa ggt ttt tat 432
 Phe Tyr Glu Ala Met Phe Ser Glu Ala Glu Lys Glu Glu Gly Phe Tyr
 130 135 140

cat caa ttc atc acg aca att caa agc gag ttt cat ggg gat gac gta 480
 His Gln Phe Ile Thr Thr Ile Gln Ser Glu Phe His Gly Asp Asp Val
 145 150 155 160

ttt tcg ctt ctt ata ggt ttg gat tat tta ctt cag aaa gat gtt aga 528
 Phe Ser Leu Leu Ile Gly Leu Asp Tyr Leu Leu Gln Lys Asp Val Arg
 165 170 175

gta aag ctc gac cag att gaa act ccc att tta ttg atc cat ggg aga 576
 Val Lys Leu Asp Gln Ile Glu Thr Pro Ile Leu Leu Ile His Gly Arg
 180 185 190

gaa gac aaa att tgt cca ctc gaa gcc tca tct ttc att aaa gaa aat 624
 Glu Asp Lys Ile Cys Pro Leu Glu Ala Ser Ser Phe Ile Lys Glu Asn
 195 200 205

ctg ggt ggg aaa gcc gag gtt cat att atc gaa ggc gct ggt cat att 672
 Leu Gly Gly Lys Ala Glu Val His Ile Ile Glu Gly Ala Gly His Ile
 210 215 220

cca ttt ttc aca aaa cca cag gaa tgt gtg cag ctt ata aaa aca ttt 720
 Pro Phe Phe Thr Lys Pro Gln Glu Cys Val Gln Leu Ile Lys Thr Phe
 225 230 235 240

att caa aag gag tac att cat gat tga 747
 Ile Gln Lys Glu Tyr Ile His Asp
 245

<210> 14

<211> 248

<212> PRT

<213> Kurthia sp.

<400> 14

Met Lys Gln Pro Asn Leu Val Met Leu Pro Gly Trp Gly Met Glu Lys
 1 5 10 15

Asp Ala Phe Gln Pro Leu Ile Lys Pro Leu Ser Glu Val Phe His Leu
 20 25 30

Ser Phe Ile Glu Trp Arg Asp Met Lys Thr Leu Asn Asp Phe Glu Glu
 35 40 45
 Arg Val Ile Asp Thr Ile Ala Ser Ile Asp Gly Pro Val Phe Leu Leu
 50 55 60
 Gly Trp Ser Leu Gly Ser Leu Leu Ser Leu Glu Leu Val Ser Ser Tyr
 65 70 75 80
 Arg Glu Lys Ile Lys Gly Phe Ile Leu Ile Gly Ala Thr Ser Arg Phe
 85 90 95
 Thr Thr Gly Asp Asn Tyr Ser Phe Gly Trp Asp Pro Arg Met Val Glu
 100 105 110
 Arg Met Lys Lys Gln Leu Gln Arg Asn Lys Glu Lys Thr Leu Thr Ser
 115 120 125
 Phe Tyr Glu Ala Met Phe Ser Glu Ala Glu Lys Glu Glu Gly Phe Tyr
 130 135 140
 His Gln Phe Ile Thr Thr Ile Gln Ser Glu Phe His Gly Asp Asp Val
 145 150 155 160
 Phe Ser Leu Leu Ile Gly Leu Asp Tyr Leu Leu Gln Lys Asp Val Arg
 165 170 175
 Val Lys Leu Asp Gln Ile Glu Thr Pro Ile Leu Leu Ile His Gly Arg
 180 185 190
 Glu Asp Lys Ile Cys Pro Leu Glu Ala Ser Ser Phe Ile Lys Glu Asn
 195 200 205
 Leu Gly Gly Lys Ala Glu Val His Ile Ile Glu Gly Ala Gly His Ile
 210 215 220
 Pro Phe Phe Thr Lys Pro Gln Glu Cys Val Gln Leu Ile Lys Thr Phe
 225 230 235 240
 Ile Gln Lys Glu Tyr Ile His Asp
 245

<210> 15

<211> 831

<212> DNA

<213> Kurthia sp.

<220>

<221> CDS

<222> (1)..(828)

<400> 15

atg att gat aaa caa ttg tta agt aag cga ttc agt gaa cat gcg aaa	48
Met Ile Asp Lys Gln Leu Leu Ser Lys Arg Phe Ser Glu His Ala Lys	
1 5 10 15	
aca tat gat gca tat gcc aat gtt caa aaa aac atg gcg aaa caa tta	96
Thr Tyr Asp Ala Tyr Ala Asn Val Gln Lys Asn Met Ala Lys Gln Leu	
20 25 30	
gtg gat ttg ctc cct caa aaa aac agc aaa caa aga att aac atc ctt	144
Val Asp Leu Leu Pro Gln Lys Asn Ser Lys Gln Arg Ile Asn Ile Leu	
35 40 45	
gaa att ggc tgc ggt act ggt tac tta acc agg tta ctc gtt aat acä	192
Glu Ile Gly Cys Gly Thr Gly Tyr Leu Thr Arg Leu Leu Val Asn Thr	
50 55 60	
ttt cct aat gct tct att acc gct gtt gat tta gca cca ggg atg gtt	240
Phe Pro Asn Ala Ser Ile Thr Ala Val Asp Leu Ala Pro Gly Met Val	
65 70 75 80	
gaa gtg gcg aaa gga ata aca atg gaa gac cgt gtt act ttt tta tgt	288
Glu Val Ala Lys Gly Ile Thr Met Glu Asp Arg Val Thr Phe Leu Cys	
85 90 95	
gct gat atc gaa gaa atg acg ctt aat gaa aat tac gac tta att att	336
Ala Asp Ile Glu Glu Met Thr Leu Asn Glu Asn Tyr Asp Leu Ile Ile	
100 105 110	
tct aat gca acg ttt caa tgg ctg aat aat ctt cct gga acc att gaa	384
Ser Asn Ala Thr Phe Gln Trp Leu Asn Asn Leu Pro Gly Thr Ile Glu	
115 120 125	
caa ttg ttt aca cga tta acg cct gaa gga aac ctg ata ttt tca acg	432
Gln Leu Phe Thr Arg Leu Thr Pro Glu Gly Asn Leu Ile Phe Ser Thr	
130 135 140	
ttt gga att aaa acc ttt caa gag ctt cat atg tcc tat gaa cat gcg	480
Phe Gly Ile Lys Thr Phe Gln Glu Leu His Met Ser Tyr Glu His Ala	
145 150 155 160	
aaa gaa aag ctt caa ctt tca att gat agt tca cca ggc caa ctg ttt	528

Lys Glu Lys Leu Gln Leu Ser Ile Asp Ser Ser Pro Gly Gln Leu Phe
165 170 175

tac gct cta gaa gaa tta tcc caa att tgt gaa gaa gca atc cct ttt 576
Tyr Ala Leu Glu Glu Leu Ser Gln Ile Cys Glu Glu Ala Ile Pro Phe
180 185 190

tca tca gca ttt cca tta gag ata aca aaa ata gaa aag ctt gaa cta 624
Ser Ser Ala Phe Pro Leu Glu Ile Thr Lys Ile Glu Lys Leu Glu Leu
195 200 205

gag tac ttt cag aca gta cgt gaa ttt ttc act tca att aaa aag att 672
Glu Tyr Phe Gln Thr Val Arg Glu Phe Phe Thr Ser Ile Lys Lys Ile
210 215 220

ggt gca gct aac agc aac aaa gaa aac tac tgc cag cgc cct tct ttt 720
Gly Ala Ala Asn Ser Asn Lys Glu Asn Tyr Cys Gln Arg Pro Ser Phe
225 230 235 240

ttt cga gag tta atc aac ata tac gaa aca aaa tac caa gat gaa tca 768
Phe Arg Glu Leu Ile Asn Ile Tyr Glu Thr Lys Tyr Gln Asp Glu Ser
245 250 255

ggt gtg aag gca acc tat cac tgt ttg ttt ttt aag ata ata aaa cat 816
Gly Val Lys Ala Thr Tyr His Cys Leu Phe Phe Lys Ile Ile Lys His
260 265 270

gcc ccc cta ccc taa 831
Ala Pro Leu Pro
275

<210> 16
<211> 276
<212> PRT
<213> Kurthia sp.

<400> 16
Met Ile Asp Lys Gln Leu Leu Ser Lys Arg Phe Ser Glu His Ala Lys
1 5 10 15

Thr Tyr Asp Ala Tyr Ala Asn Val Gln Lys Asn Met Ala Lys Gln Leu
20 25 30

Val Asp Leu Leu Pro Gln Lys Asn Ser Lys Gln Arg Ile Asn Ile Leu
35 40 45

Glu Ile Gly Cys Gly Thr Gly Tyr Leu Thr Arg Leu Leu Val Asn Thr

50	55	60
Phe Pro Asn Ala Ser Ile Thr Ala Val Asp Leu Ala Pro Gly Met Val		
65	70	75 80
Glu Val Ala Lys Gly Ile Thr Met Glu Asp Arg Val Thr Phe Leu Cys		
	85	90 95
Ala Asp Ile Glu Glu Met Thr Leu Asn Glu Asn Tyr Asp Leu Ile Ile		
100	105	110
Ser Asn Ala Thr Phe Gln Trp Leu Asn Asn Leu Pro Gly Thr Ile Glu		
115	120	125
Gln Leu Phe Thr Arg Leu Thr Pro Glu Gly Asn Leu Ile Phe Ser Thr		
130	135	140
Phe Gly Ile Lys Thr Phe Gln Glu Leu His Met Ser Tyr Glu His Ala		
145	150	155 160
Lys Glu Lys Leu Gln Leu Ser Ile Asp Ser Ser Pro Gly Gln Leu Phe		
	165	170 175
Tyr Ala Leu Glu Glu Leu Ser Gln Ile Cys Glu Glu Ala Ile Pro Phe		
180	185	190
Ser Ser Ala Phe Pro Leu Glu Ile Thr Lys Ile Glu Lys Leu Glu Leu		
195	200	205
Glu Tyr Phe Gln Thr Val Arg Glu Phe Phe Thr Ser Ile Lys Lys Ile		
210	215	220
Gly Ala Ala Asn Ser Asn Lys Glu Asn Tyr Cys Gln Arg Pro Ser Phe		
225	230	235 240
Phe Arg Glu Leu Ile Asn Ile Tyr Glu Thr Lys Tyr Gln Asp Glu Ser		
	245	250 255
Gly Val Lys Ala Thr Tyr His Cys Leu Phe Phe Lys Ile Ile Lys His		
260	265	270
Ala Pro Leu Pro		
275		

<210> 17

<211> 360

<212> DNA
 <213> Kurthia sp.

 <220>
 <221> RBS
 <222> Complement((67)..(76))

 <220>
 <221> -35_signal
 <222> (210)..(215)

 <220>
 <221> -10_signal
 <222> (234)..(239)

 <220>
 <221> -10_signal
 <222> Complement((235)..(240))

 <220>
 <221> RBS
 <222> (289)..(293)

 <220>
 <221> misc_feature
 <222> (302)..(358)
 <223> Partial sequence of ORF2.

 <220>
 <221> misc_feature
 <222> (125)..(164)
 <223> BOX1 - inverted repeat

 <220>
 <221> misc_feature
 <222> (244)..(283)
 <223> BOX2 - inverted repeat

 <220>
 <221> misc_feature
 <222> Complement((1)..(58))
 <223> Partial sequence of ORF1.

<400> 17
 cgccaatggc agttaacgca gtaaataagg caacataaga gatcgtttta gctttcaagt 60
 tttcaacctc ctttttttaa aattggtagg taaaatgccc actattagtg tgcattgatt 120
 atatattata tgtcaaccat ttattatttt agttaacata taaagcgcaa taaaatgac 180
 agacttagaa aaatattgaa aattagtaat tgaacaatat tttatttggtg tggtattata 240

caatttatat gttaactatt ttaagatata gttaacatat aaaggcttgg agggacaaca 300
tatgacagga gaaatgttaa tacaggatga actttccaga gaaacagcgg tatttgtggc 360

<210> 18

<211> 20

<212> PRT

<213> Kurthia sp.

<400> 18

Leu Lys Ala Lys Thr Ile Ser Tyr Val Ala Leu Phe Thr Ala Leu Thr
1 5 10 15

Ala Ile Gly Ala

20

<210> 19

<211> 20

<212> PRT

<213> Kurthia sp.

<400> 19

Met Thr Gly Glu Met Leu Ile Gln Asp Glu Leu Ser Arg Glu Thr Ala
1 5 10 15

Val Phe Val Ala

20

<210> 20

<211> 240

<212> DNA

<213> Kurthia sp.

<220>

<221> -35_signal

<222> (65)..(70)

<220>

<221> -10_signal

<222> (91)..(96)

<220>

<221> RBS

<222> (127)..(135)

<220>

<221> CDS

<222> (142)..(240)

<223> bioH

<400> 20

actaaccct atggtgtcca gattaagcgt aatgtagtat aggatttttag tcaattagca 60

atTTTTgaaa tatttagtac gatcacataa tagaatcata tataatgatt aaaatattaa 120

ttacagaaaa gaggtatttt c atg cca ttc gta aat cat gac aat gaa agc 171

Met Pro Phe Val Asn His Asp Asn Glu Ser

1 5 10

ctt tac tat gag gtt cac gga caa ggt gat cct tta ttg ttg att atg 219

Leu Tyr Tyr Glu Val His Gly Gln Gly Asp Pro Leu Leu Leu Ile Met

15 20 25

ggg ctc ggc tat aac tct tta 240

Gly Leu Gly Tyr Asn Ser Leu

30

<210> 21

<211> 33

<212> PRT

<213> Kurthia sp.

<400> 21

Met Pro Phe Val Asn His Asp Asn Glu Ser Leu Tyr Tyr Glu Val His

1 5 10 15

Gly Gln Gly Asp Pro Leu Leu Leu Ile Met Gly Leu Gly Tyr Asn Ser

20 25 30

Leu

<210> 22

<211> 300

<212> DNA

<213> Kurthia sp.

<220>

<221> -35_signal

<222> (83)..(88)

<220>
<221> -10_signal
<222> (107)..(112)

<220>
<221> misc_feature
<222> (115)..(154)
<223> Box 3 - inverted repeat

<220>
<221> RBS
<222> (154)..(161)

<220>
<221> misc_feature
<222> (168)..(299)
<223> Partial sequence of bioFII (full gene is SEQ ID
NO: 11).

<400> 22
ttatgataag tgtctttttt cgcccttga tttctcctag attaatggat aatcaattta 60
ttatcatggt ctttttcaaa gcttgacagt ttcattgagt catgattaga atgttttata 120
tgттаaccta tattattttt agttaacata taaaaaggag aatggctatg cacagtgaaa 180
aacaattacc ttgttgggaa gaaaaaatta agaaagaact ggcttattta gaagagatat 240
cgcaaaaacg tgaactcggt tcaacggaat tcgccgagca gccatggctt atgatcaacg 300

<210> 23
<211> 45
<212> PRT
<213> Kurthia sp.

<400> 23
Met His Ser Glu Lys Gln Leu Pro Cys Trp Glu Glu Lys Ile Lys Lys
1 5 10 15
Glu Leu Ala Tyr Leu Glu Glu Ile Ser Gln Lys Arg Glu Leu Val Ser
20 25 30
Thr Glu Phe Ala Glu Gln Pro Trp Leu Met Ile Asn Gly
35 40 45